

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: February 26, 2002, 07:51:23 ; Search time 202.3 Seconds

(without alignments)
4729.486 Million cell updates/sec

Title: US-09-602-833a-1

Perfect score: 1116

Sequence: 1 atggacataaagtgtgttgc.....ctttagccttcaatttga 1116

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapect 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : N.Geneseq_1101.*
1: /SIDS2/gcgdata/geneseq/NA1980.DAT.*
2: /SIDS2/gcgdata/geneseq/NA1981.DAT.*
3: /SIDS2/gcgdata/geneseq/NA1982.DAT.*
4: /SIDS2/gcgdata/geneseq/NA1983.DAT.*
5: /SIDS2/gcgdata/geneseq/NA1984.DAT.*
6: /SIDS2/gcgdata/geneseq/NA1985.DAT.*
7: /SIDS2/gcgdata/geneseq/NA1986.DAT.*
8: /SIDS2/gcgdata/geneseq/NA1987.DAT.*
9: /SIDS2/gcgdata/geneseq/NA1988.DAT.*
10: /SIDS2/gcgdata/geneseq/NA1989.DAT.*
11: /SIDS2/gcgdata/geneseq/NA1990.DAT.*
12: /SIDS2/gcgdata/geneseq/NA1991.DAT.*
13: /SIDS2/gcgdata/geneseq/NA1992.DAT.*
14: /SIDS2/gcgdata/geneseq/NA1993.DAT.*
15: /SIDS2/gcgdata/geneseq/NA1994.DAT.*
16: /SIDS2/gcgdata/geneseq/NA1995.DAT.*
17: /SIDS2/gcgdata/geneseq/NA1996.DAT.*
18: /SIDS2/gcgdata/geneseq/NA1997.DAT.*
19: /SIDS2/gcgdata/geneseq/NA1998.DAT.*
20: /SIDS2/gcgdata/geneseq/NA1999.DAT.*
21: /SIDS2/gcgdata/geneseq/NA2000.DAT.*
22: /SIDS2/gcgdata/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1116	100.0	1116	AAF24902	Nucleotide sequence
2	681	61.0	681	AAF24903	Nucleotide sequence
3	130.4	11.7	2056	AAH17218	Human cDNA sequenc
4	92.8	8.3	936	AAF58252	Oligonucleotide D1
5	92.8	8.3	936	AAF58254	Oligonucleotide D1
6	92.8	8.3	936	AAF58257	Oligonucleotide D1
7	92.8	8.3	936	AAF58259	Oligonucleotide D2
8	92.8	8.3	936	AAF58262	Oligonucleotide D2
9	92.8	8.3	936	AAF58255	Oligonucleotide D1
10	92.6	8.3	936	AAF58252	Oligonucleotide D1
11	92.6	8.3	936	AAF58254	Oligonucleotide D1

12	92.6	8.3	936	AAF58257	Oligonucleotide D1
13	92.6	8.3	936	AAF58259	Oligonucleotide D2
14	92.6	8.3	936	AAF58262	Oligonucleotide D2
15	92.6	8.3	938	AAF58255	Oligonucleotide D1
16	63.2	5.7	2840	AAH24230	Human Ras-binding
17	63.2	5.7	2847	AAH17735	Human cDNA sequenc
18	57.4	5.1	1600	AA161075	Human polynucleoti
19	57.4	5.1	1947	AAH52247	Protein PRO239 cDN
20	57.4	5.1	1947	AAH72405	Human PRO239 cDNA
21	57.4	5.1	2384	AAH30919	Human secreted pro
22	57.4	5.1	2384	AAH8398	Human cDNA clone A
23	57.4	5.1	2412	AA159289	Human polynucleoti
24	57.4	5.1	2641	AA552427	HTM clone 2709055
25	56.8	5.1	6242	AAH94945	Human cDNA encodin
26	55.8	5.0	2410	AAH41479	Human cDNA sequenc
27	55.8	5.0	5199	AA158154	Human polynucleoti
28	55.2	4.9	3159	AAH99494	Human DNA encoding
29	55.2	4.9	3400	AAH72745	Human ORFX ORF2153
30	55.2	4.9	6125	AAH14529	Human cervical can
31	53.2	4.8	2620	AAH14529	Human cDNA sequenc
32	52.6	4.7	3138	AAH30202	Human RING finger
33	51.8	4.6	495	AAH61814	CDNA encoding mult
34	51.8	4.6	495	AAH61814	Skin cell cDNA, SE
35	51.8	4.6	2169	AAH30203	Human RING finger
36	51.8	4.6	2169	AAH30203	DNA encoding human
37	51.8	4.6	6470	AAH58376	Human polynucleoti
38	50.4	4.5	2527	AAH15457	Human cDNA sequenc
39	49.8	4.5	2694	AAH45671	Nucleotide sequenc
40	49.8	4.4	502	AAH00229	Human secreted pro
41	49.8	4.4	3938	AAH33095	Murine p53-induced
42	48.8	4.4	1710	AAH33095	Human colon cancer
43	48.8	4.3	528	AAH06111	Human cDNA clone (
44	46.8	4.2	3205	AAH34518	Death activator de
45	46.2	4.1	861	AAH06813	Human cDNA clone (

ALIGNMENTS

RESULT 1	
AAF24902	AAF24902 standard; cDNA; 1116 BP.
XX	XX
AC	AAF24902:
XX	XX
DT	20-APR-2001 (first entry)
XX	XX
DE	Nucleotide sequence of a human SGT4.1 polypeptide.
XX	XX
KW	Human: SGT4; signal transduction; guanosine triphosphate binding protein;
KW	GTP binding protein; cancer; immune response; nutritional source;
KW	animal feed; ss.
XX	XX
OS	Homo sapiens.
XX	XX
FH	Key
FT	1..1116
FT	/*tag= a
FT	/product= "SGT4"
XX	XX
PN	WO200078959-A1.
XX	XX
PD	28-DEC-2000.
XX	XX
PF	22-JUN-2000; 2000WO-US17248.
XX	XX
PR	23-JUN-1999; 99US-0140627.
XX	XX
PA	(LEXI-) LEXICON GENETICS INC.
XX	XX
PI	Turner AC, Zambrowicz B, Nehls M, Friedrich GA, Sands AT;
XX	XX
DR	WPI; 2001-032329/04.

[illegible]

Oy	439	agaattcggtcgcgaataaaccaatccacacttccagaaatcggltcttg	498
Dd	668	ww	629
Oy	499	aagaacctgaaagactaatgtggtttcaactatctgaagacatctctccaagt	558
Dd	628	ww	569
Oy	559	ggagattgtgaatatctaagagacgtgatgtgtcttcgaaaactagaataatcggagctg	618
Dd	568	ww	509
Oy	619	coccttgaattgaatlaattgaagcaagttacattgttagatalccgaacaagt	678
Dd	508	ww	449
Oy	679	tccagtgccccaatctgttctcctgcgagtgctgaattgcagtggtgtgatalccagcgc	738
Dd	448	ww	389
Oy	739	aataacctgaccgacctgcgcaagataatagacagcctagaaggagctgcagagcttctc	798
Dd	388	ww	329
Oy	799	tgtgtaaaaaaagaatgbagctaccctcccatctccatctgctgaacctgaaagactcac	858
Dd	328	ww	269
Oy	859	ctgtatgcgtcagtgvggacatttgttggagctcccacgtcccttgtgactatcc	918
Dd	268	ww	209
Oy	919	acaaccttaaatctgttaagccttatggaacatccctattgataatgcccaatgtgaagat	978
Dd	208	ww	149
Oy	979	ggcaatgaataatggaagaggaacggagatcgccaacatttgttaaagaattatgaa	1033
Dd	148	ww	89
Oy	1039	gcatatattgaagacctaaagaagaatctgttccacgatalaccaccaagtgtct	1099
Dd	88	ww	29
Oy	1099	tttagccttcaactt 1114	
Dd	28	wwwwwwwwwwwwwwwwww 13	
 RESULT 5 AAFS8254/C ID AAF58254 standard; DNA; 936 BP. XX AAF58254; AC AAF58254; XX DT 24-APR-2001 (first entry) XX DE Oligonucleotide D1875. XX KM Electon-transfer group; ETM; mismatch; genotyping; KW gene expression; ss. XX OS Synthetic. XX PN WO200107665-A2. XX PD 01-FEB-2001. XX PF 26-JUL-2000; 2000WO-US20476. PR 26-JUL-1999; 99US-0145695. PR 17-MAR-2000; 2000US-0190259. XX			

559 aaattatataaaactaatctaatctaaaatatataaacctc 618

PT Nucleic acids containing electron-transfer group, useful as labels in

PT Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface -
XX

SQ	Sequence	936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;
Query Match	8.3%; Score 92.6; DB 22; Length 936;	
Best Local Similarity	0.7%; Pred. No. 6e-18;	
Matches	5; Conservative 441; Mismatches 295; Indels 0; Gaps 0;	
QY	374aatggtacataagaactccttgattcaatcatctccatataatatccaagtatttcaaag	433
Dd	10#####	69
QY	434cgatgagaatctctgatctgcgaaaaaaaccaatctcacatcttcagcagaatcggtt	493
Dd	70#####	129
QY	494gtttgaagaacctgaagaactcaatctgggtttacaatctctgaagaactctctcag	553
Dd	130#####	189
QY	554aatggagatctgtaaaatctagaagagactgattgtcttgaaatctagaattaatg	613
Dd	190#####	249
QY	614agctgcctcttgaattaagtaattggaagcagttaccatttgttagatalctcaagaanaa	673
Dd	250#####	309
QY	674agtttccagttcccacaatctgtctcctcgatgcagatgttcgaatttcagttgtgatca	733

RESULT 12	
AAF58257	
ID	AAF58257 standard; DNA; 936 BP.
XX	
AC	AAF58257;
XX	
DT	24-APR-2001 (first entry)
XX	
DE	Oligonucleotide D1954.
XX	
KW	Electron-transfer group; ETW; mismatch; genotyping;
KW	gene expression; ss.
XX	

OS Synthetic.
 XX WO200107665-A2.
 XX
 XX 01-FEB-2001.
 PD
 XX 26-JUL-2000; 2000WO-US20476.
 PF
 XX 26-JUL-1999; 99US-0145695.
 PR 17-MAR-2000; 2000US-0190259.
 XX
 PA (CLIN-) CLINICAL MICRO SENSORS INC.
 XX
 PI Umek RM;
 XX
 DR WPI: 2001-159728/16.
 XX
 PT Nucleic acids containing electron-transfer group, useful as labels in
 PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
 PT a single surface
 PS
 XX Example 6; Page 127; 159pp; English.
 XX
 CC The present invention relates to a composition comprising two nucleic
 CC acids each containing an electron-transfer group (ETM) having
 CC different redox potentials. The invention is used for electronic
 CC detection of nucleic acids, especially of substitutions (mismatches)
 CC and single-nucleotide polymorphisms, e.g. for genotyping,
 CC monitoring gene expression.
 XX
 XX Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;

Query Match 8.3%; Score 92.6; DB 22; Length 936;
 Best Local Similarity 0.7%; Pred. No. 6e-18;
 Matches 5; Conservative 441; Mismatches 295; Indels 0; Gaps 0;

OY 374 aatggtacataagcaatccttgatccaatcctcctacatataatcgtatttcaag 433
 DB 10 www.
 OY 434 cgatgagaattcgtatcgcacaaacacacatcctacatctccagcagaatcggtt 493
 DB 70 www.
 OY 494 gtttgaagaacctgaagaactcaatggtttcaactatctgaagagactcctccag 553
 DB 130 www.
 OY 554 aattggagattgtgaaatctagagagactgattgttctcgtgaaatcagaattatg 613
 DB 190 www.
 OY 614 agctgccttgaacttaatttgaagcaagtacattgttagatatcctcagcaaaa 673
 DB 250 www.
 OY 674 agtttccagtgcccaatctgttcctcgtgagtgatgcaattgagtggtgatata 733
 DB 310 www.
 OY 734 gcagcaataactgacgcagctgcgcaagatatagacagctagagagctgcagact 793
 DB 370 www.
 OY 794 ttctcttgataaaaaaagtgtgacctcctcctatcctcagtgcaaccgaagaac 853
 DB 430 www.
 OY 854 tcaactcgttagtcgtagtgagacattgttgtagctcccaactgcctttagact 913
 DB 450 www.

OY 914 catcacaccttaaaattgtgaagccttatgagacaatcctctgataatgcccaatg 973
 DB 550 www.
 OY 974 aagatggcaatgaataatgaaatgaaagcgatcgccacatttgaagaagta 1033
 DB 610 www.
 OY 1034 tgaagcctataatgaagaccttaagaagaagactgttccagctataccaccaag 1093
 DB 670 www.
 OY 1094 tgcctttagccttcaactt 1114
 DB 730 www.

RESULT 13
 AAF58259
 ID AAF58259 standard; DNA: 936 BP.

AAF58259;
 24-APR-2001 (first entry)
 DE Oligonucleotide D2004.
 XX
 XX Electron-transfer group; ETM; mismatch; genotyping;
 KW gene expression; ss.
 XX
 OS Synthetic.
 XX
 XX WO200107665-A2.
 XX
 XX 01-FEB-2001.
 PD
 XX 26-JUL-2000; 2000WO-US20476.
 PF
 XX 26-JUL-1999; 99US-0145695.
 PR 17-MAR-2000; 2000US-0190259.
 XX
 PA (CLIN-) CLINICAL MICRO SENSORS INC.
 XX
 PI Umek RM;
 XX
 DR WPI: 2001-159728/16.
 XX
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 PS
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 CC different redox potentials. The invention is used for electronic
 CC detection of nucleic acids, especially of substitutions (mismatches)
 CC and single-nucleotide polymorphisms, e.g. for genotyping,
 CC monitoring gene expression.

Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other;

Query Match 8.3%; Score 92.6; DB 22; Length 936;
 Best Local Similarity 0.7%; Pred. No. 6e-18;
 Matches 5; Conservative 441; Mismatches 295; Indels 0; Gaps 0;

OY 374 aatggtacataagcaatccttgatccaatcctcctacatataatcgtatttcaag 433
 DB 10 www.
 OY 434 cgatgagaattcgtatcgcacaaacacacatcctacatctccagcagaatcggtt 493
 DB 450 www.

Db 70 www..... 129
QY 494 gtttgaagaacctgaactgaatgtgggttcaatactctgaagaagcttccctcag 553
Db 130 www..... 189
QY 554 aattggagattgtgaatactagagagactgattctctggaactgataatga 613
Db 190 www..... 249
QY 614 agctgaccttgaataaattgaagaagttacattttagatactcagaaca 673
Db 250 www..... 309
QY 674 agtttccagtgcccaatctgtcctcgagatgcgaatttgcaatgtgttatca 733
Db 310 www..... 369
QY 734 gcagcaataacctgacacctgcgcgaagatagacagctagagagctgagagct 793
Db 370 www..... 429
QY 794 ttctctgtataaacaagttgacctacttccctatccatgtcgaacctgaagaagc 853
Db 430 www..... 489
QY 854 tcaactcgttagtcgtcagtgaggacatttgtgtgagctcccaactgaccttgtact 913
Db 490 www..... 549
QY 914 catcacacctttaaattgttaagccttatgacaatcctattgataatgcacatgtg 973
Db 550 www..... 609
QY 974 aagatggcaatgaataatggaagtgacggagatcgccaacattttagataaagaagta 1033
Db 610 www..... 669
QY 1034 tgaagcctatatggaagccttaagaagaagatctgttccagctatacccaaga 1093
Db 670 www..... 729
QY 1094 tgtctttagcctcaactt 1114
Db 730 www..... 750

RESULT 14

AAF58262
ID AAF58262 standard; DNA; 936 BP.
XX
AC AAF58262;
XX
DT 24-APR-2001 (first entry)
XX
DE Oligonucleotide D2007.
XX
KM Electron-transfer group; ETM; mismatch; genotyping;
KW gene expression; ss.
XX
OS Synthetic.
XX
PN MO200107665-A2.
XX
PD 01-FEB-2001.
XX
PF 26-JUL-2000; 2000MO-US20476.
XX
PR 26-JUL-1999; 99US-0145695.
XX
PR 17-MAR-2000; 2000US-0190259.
XX
PA (CLIN-) CLINICAL MICRO SENSORS INC.
XX

PI Unk RM;
XX
DR WPI; 2001-159728/16.
XX
PT Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface -
XX
PS Example 6; Page 128; 159pp; English.
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CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
SQ Sequence 936 BP; 5 A; 139 C; 10 G; 6 T; 776 other;

Query Match 8 3%; Score 92.6; DB 22; Length 936;
Best Local Similarity 0.7%; Pred. No. 6e-18; 295; Indels 0; Gaps 0;
Matches 5; Conservative 44; Mismatches 295; Indels 0; Gaps 0;

QY 374 aatgtacataagcaataaccttgattccaatcattccatataatcaatttcaag 433
Db 10 www..... 69
QY 434 cgaatgaatctgtagctgcgaataaacaatccaatccaatcctccagcagaatcggt 493
Db 70 www..... 129
QY 494 gtttgaagaacctgaactgaatgtgggttcaatactctgaagaagcttccctcag 553
Db 130 www..... 189
QY 554 aattggagattgtgaatactagagagactgattctctggaactgataatga 613
Db 190 www..... 249
QY 614 agctgaccttgaataaattgaagaagttacattttagatactcagaaca 673
Db 250 www..... 309
QY 674 agtttccagtgcccaatctgtcctcgagatgcgaatttgcaatgtgttatca 733
Db 310 www..... 369
QY 734 gcagcaataacctgacacctgcgcgaagatagacagctagagagctgagagct 793
Db 370 www..... 429
QY 794 ttctctgtataaacaagttgacctacttccctatccatgtcgaacctgaagaagc 853
Db 430 www..... 489
QY 854 tcaactcgttagtcgtcagtgaggacatttgtgtgagctcccaactgaccttgtact 913
Db 490 www..... 549
QY 914 catcacacctttaaattgttaagccttatgacaatcctattgataatgcacatgtg 973
Db 550 www..... 609
QY 974 aagatggcaatgaataatggaagtgacggagatcgccaacattttagataaagaagta 1033
Db 610 www..... 669
QY 1034 tgaagcctatatggaagccttaagaagaagatctgttccagctatacccaaga 1093
Db 670 www..... 729
QY 1094 tgtctttagcctcaactt 1114

```
Db 730 ..... 750
RESULT 15
AAF58255
ID AAF58255 standard; DNA; 938 BP.
XX
AC AAF58255;
XX
DT 24-APR-2001 (first entry)
XX
DE Oligonucleotide D1876.
XX
KM Electron-transfer group; ETM; mismatch; genotyping;
KM gene expression; ss.
XX
OS Synthetic.
XX
PN W0200107665-A2.
XX
PD 01-FEB-2001.
XX
PE 26-JUL-2000; 2000WO-US20476.
XX
PR 26-JUL-1999; 99US-0145695.
PR 17-MAR-2000; 2000US-0190259.
XX
PA (CLIN-) CLINICAL MICRO SENSORS INC.
XX
PI Unemk RM;
XX
DR WPI; 2001-159728/16.
XX
PT Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
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XX
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CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
SQ Sequence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other;

Query Match 8.3%; Score 92.6; DB 22; Length 938;
Best Local Similarity 0.7%; Pred. NO. 6e-18;
Matches 5; Conservative 441; Mismatches 295; Indels 0; Gaps 0;

QY 374 aatggtacataagaataccttgatccaataatcctacatctccagcagaatcggt 433
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 10 ..... 69
QY 434 cgatgagaattcgtatctgcacaaacaaatcctacatctccagcagaatcggt 493
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 70 ..... 129
QY 494 gttgaagaacctgaagaactcaatgtgggttcaactatcgaagacatctccag 553
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 130 ..... 189
QY 554 aatggagagattcgtaaaatctagagagactggttctggaatctagaatgaatg 613
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 190 ..... 249
QY 614 agctgccttgtaattgaatgaagcaagttacattgtgatctccagcaaca 673
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 250 ..... 309
```

```
QY 674 agttccagtgcccaactcgtgtcctcgagatgctgaatttgagtggttgatalca 733
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 310 ..... 369
QY 734 gcagcaataacctgcgacctgcgcgaagatatagacagctagagagctgcagagct 793
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 370 ..... 429
QY 794 ttctcttgataaaacaaagttgacctctccatccatctgatgctgaacctgaagaagc 853
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 430 ..... 489
QY 854 tcaactgttagtcgtcagtgaggacatttggltgagctcccaactgccttggact 913
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 490 ..... 549
QY 914 catccacaccttaaatctgaagcctatggaacatccatgtatatagcccaatgtg 973
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 550 ..... 609
QY 974 aagatgcaatgaaataatggaagtgaacggaatcgcccaactttgataagaagta 1033
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 610 ..... 669
QY 1034 tgaagcctatattgaagaccttaagaagaagaatctgttccagctataccaccaag 1093
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 670 ..... 729
QY 1094 tgccttgaagcctcaactt 1114
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 730 ..... 750
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Search completed: February 26, 2002, 10:47:40
Job time: 10577 sec